

PCT09

KW

RAW SEQUENCE LISTING

DATE: 06/22/2001

PATENT APPLICATION: US/09/786,442A

TIME: 10:35:42

Input Set : A:\ES.txt

Output Set: N:\CRF3\06222001\I786442A.raw

ENTERED

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3 <110> APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
4     TAKAHASHI, Tsuneo
5     ONO, Mitsuharu
6     ISHIMARU, Hiroshi
7     KANNO, Kimiyoshi
8     TAKAHASHI, Chiaki
10 <120> TITLE OF INVENTION: Novel receptor protein and method for the diagnosis of an
11     inflammatory disease by using the same
13 <130> FILE REFERENCE: 99-1043
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/786,442A
C--> 15 <141> CURRENT FILING DATE: 2001-05-17
15 <150> PRIOR APPLICATION NUMBER: JP 10-249752
16 <151> PRIOR FILING DATE: 1998-09-03
18 <150> PRIOR APPLICATION NUMBER: JP 11-070800
19 <151> PRIOR FILING DATE: 1999-03-16
21 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04801
22 <151> PRIOR FILING DATE: 1999-09-03
24 <160> NUMBER OF SEQ ID NOS: 12
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1014
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)...(1011)
35 <400> SEQUENCE: 1
36 atg ggg aac gat tct gtc agc tac gag tat ggg gat tac agc gac ctc      48
37 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
38   1           5           10           15
39 tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg gcc atc gac      96
40 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
41           20           25           30
42 ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc ttc ctg gtg      144
43 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
44           35           40           45
45 ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg aag gtg gcc      192
46 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
47   50           55           60
48 cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc gtg gcg gat      240
49 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
50   65           70           75           80
51 ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc att gcc cgt      288
52 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
53           85           90           95
54 gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg ctg ccc tcc      336
55 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
56           100           105           110
57

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```

58 atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg gca gct ctc 384
59 ile ile leu leu thr met tyr ala ser val leu leu leu ala ala leu
60      115      120      125
61 agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg tgg tct acg 432
62 ser ala asp leu cys phe leu ala leu gly pro ala trp trp ser thr
63      130      135      140
64 gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca gcc tgg aca 480
65 val gln arg ala cys gly val gln val ala cys gly ala ala trp thr
66 145      150      155      160
67 ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc cgg ctg cac 528
68 leu ala leu leu leu thr val pro ser ala ile tyr arg arg leu his
69      165      170      175
70 cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac tac ggc ggc 576
71 gln glu his phe pro ala arg leu gln cys val val asp tyr gly gly
72      180      185      190
73 tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt ctt ttt ggc 624
74 ser ser ser thr glu asn ala val thr ala ile arg phe leu phe gly
75      195      200      205
76 ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt gcc ctc ctg 672
77 phe leu gly pro leu val ala val ala ser cys his ser ala leu leu
78      210      215      220
79 tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc att gtg gtg 720
80 cys trp ala ala arg arg cys arg pro leu gly thr ala ile val val
81 225      230      235      240
82 ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg ctg gtg ctc 768
83 gly phe phe val cys trp ala pro tyr his leu leu gly leu val leu
84      245      250      255
85 act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc ctg cgg gct 816
86 thr val ala ala pro asn ser ala leu leu ala arg ala leu arg ala
87      260      265      270
88 gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc ctc aat ccc 864
89 glu pro leu ile val gly leu ala leu ala his ser cys leu asn pro
90      275      280      285
91 atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg tca ctg cca 912
92 met leu phe leu tyr phe gly arg ala gln leu arg arg ser leu pro
93      290      295      300
94 gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag gac gaa agt 960
95 ala ala cys his trp ala leu arg glu ser gln gly gln asp glu ser
96 305      310      315      320
97 gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg gag atg gag 1008
98 val asp ser lys lys ser thr ser his asp leu val ser glu met glu
99      325      330      335
101 gtg tag 1014
102 val
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 337
107 <212> TYPE: PRT
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 2

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111 Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
112 1 5 10 15
113 Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
114 20 25 30
115 Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
116 35 40 45
117 Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
118 50 55 60
119 Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
120 65 70 75 80
121 Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
122 85 90 95
123 Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
124 100 105 110
125 Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
126 115 120 125
127 Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
128 130 135 140
129 Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
130 145 150 155 160
131 Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
132 165 170 175
133 Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
134 180 185 190
135 Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
136 195 200 205
137 Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
138 210 215 220
139 Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
140 225 230 235 240
141 Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
142 245 250 255
143 Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
144 260 265 270
145 Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
146 275 280 285
147 Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
148 290 295 300
149 Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
151 305 310 315 320
152 Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
153 325 330 335
154 Val
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 1287
159 <212> TYPE: DNA
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 3
163 cctgtgtgcc acgtgctgga caaatcttaa ctctcaagg actcccaaaa ccagagacac 60

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164 caggagcctg aatggggaac gattctgtca gctacgagta tggggattac agcgacctct 120
165 cggaccgccc tgtggactgc ctggatggcg cctgcctggc catcgaccgc ctgcgcgtgg 180
166 ccccgctccc actgtatgcc gccatcttcc tggtaggggt gccgggcaat gccatggtgg 240
167 cctgggtggc tgggaagggt gcccgccgga gggtaggtgc cacctgggtg ctccacctgg 300
168 ccgtggcgga tttgctgtgc tgtttgtctc tgcccatcct ggcagtggcc attgcccgtg 360
169 gagggcactg gccgtatggt gcagtgggct gtcgggctgc gccctccatc atcctgctga 420
170 ccatgtatgc cagcgtcctg ctctggcag ctctcagtgc cgacctctgc ttctggctc 480
171 tcgggcctgc ctggtggtct acggttcagc gggcgtgcgg ggtgcagggt gcctgtgggg 540
172 cagcctggac actggccttg ctgctaccgc tgccctccgc catctaccgc cggctgcacc 600
173 aggagcactt cccagcccgg ctgcagtgtg tggtaggacta cggcggtccc tccagcaccg 660
174 agaatgcggg gactgccatc cggtttcttt ttggttccct ggggcccctg gtggccgtgg 720
175 ccagctgcca cagtgccttc ctgtgctggg cagcccgacg ctgcccggcg ctgggcacag 780
176 ccattgtggt ggggtttttt gtctgctggg caccctacca cctgctgggg ctggtgctca 840
177 ctgtggcggc cccgaactcc gcaactcctg ccagggccct gcgggctgaa cccctcatcg 900
178 tgggccttgc cctcgtcac agctgcctca atcccatgct ctctctgtat tttgggaggg 960
179 ctcaactccg ccggtcactg ccagctgcct gtcactgggc cctgaggagg tcccagggcc 1020
180 aggacgaaag tgtggacagc aagaaatcca ccagccatga cctggtctcg gagatggagg 1080
181 tgtaggctgg agagacattg tgggtgtgta tcttcttacc tcatcttaca agactggcct 1140
182 caggcatagc tggatccagg agctcaatga tgtcttcatt ttattccttc cttcattcaa 1200
183 cagatatcca tcatgcactt gctatgtgca aggccttttt aggcactaga gatatagcag 1260
184 tgaccaaaac agacacaaat cctgccc 1287

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187 <210> SEQ ID NO: 4

188 <211> LENGTH: 1287

189 <212> TYPE: DNA

190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 4

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193 gggcaggatt tgtgtctgtt ttggtcactg ctatatctct agtgcctaaa aaggccttgc 60
194 acatagcaag tgcattgatg atatctgttg aatgaaggaa ggaataaaat gaagacatca 120
195 ttgagctcct ggatccagct atgcttgaag ccagtcctgt gaaatgagat aagaagatac 180
196 acaccacaaa tgtctctcca gcctacacct ccatctccga gaccaggcca tggctggtgg 240
197 atttcttctg gtccacactt tcgtcctggc cctgggactc cctcaggggc cagtgcagg 300
198 cagctggcag tgaccggcgg agttgagccc tcccacaaata cagggaagagc atgggattga 360
199 ggcagctgtg agcagaggca aggccacga tgaggggttc agcccgcagg gccctggcca 420
201 ggagtgcgga gttcggggcc gccacagtga gcaccagccc cagcagggtg tagggtgccc 480
202 agcagacaaa aaaccccacc acaatggctg tgcccagcgg ccggcagcgt cgggctgccc 540
203 agcacaggag ggcactgttg cagctggcca cggccaccag gggcccagg aagccaaaaa 600
204 gaaaccggat ggcattcacc gcattctcgg tgctggagga gccgcccgtg tccaccacac 660
205 actgcagccg ggctgggaag tgcctcgtgt gcagccggcg gtagatggcg gagggcacag 720
206 tgagcagcaa ggccagtgtc caggctgccc cacaggccac ctgcaccccg cagcccgcgt 780
207 gaaccgtaga ccaccaggca ggcccagag ccaggaagca gaggtcggca ctgagagctg 840
208 ccaggagcag gacgtgtgca tacatggtca gcaggatgat ggagggcagc gcccgacagc 900
209 cactgcacc atacggccag tggcctccac gggcaatggg cactgccagg atgggcagag 960
210 aaaaacagca cagcaaatcc gccacggcca ggtggagcaa ccagggtggca cccaccctcc 1020
211 ggcggggccac ctccccagcc acccaggcca ccatggcatt gcccggcacc cccaccagga 1080
212 agatggcggc atacagtggg agcggggcga cgcgcagcgg gtcgatggcc aggcaggcgc 1140
213 catccaggca cccacaggg cggtccgaga ggtcgtgtga atcccatac tcgtagctga 1200
214 cagaatcgtt ccccatcag gctcctggtg tctctggttt tgggagtcct tgaggagtta 1260
215 agatttgtcc agcacgtggc acacagg 1287

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218 <210> SEQ ID NO: 5

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219 <211> LENGTH: 30
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
W--> 224 <221> NAME/KEY: modified base
225 <222> LOCATION: 18
226 <223> OTHER INFORMATION: i
228 <220> FEATURE:
W--> 229 <221> NAME/KEY: modified base
230 <222> LOCATION: 22
231 <223> OTHER INFORMATION: i
233 <220> FEATURE:
W--> 234 <221> NAME/KEY: modified base
235 <222> LOCATION: 24
236 <223> OTHER INFORMATION: i
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of
240 conventional
241 7-pass transmembrane receptor proteins which are considered to
242 participate in the proliferation of melanoma
245 <400> SEQUENCE: 5
W--> 246 atcttaagct tgaacctngc cntngcdgac 30
249 <210> SEQ ID NO: 6
251 <211> LENGTH: 33
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
W--> 256 <221> NAME/KEY: misc difference
257 <222> LOCATION: 21
258 <223> OTHER INFORMATION: a, g, c or t
260 <220> FEATURE:
W--> 261 <221> NAME/KEY: modified base
262 <222> LOCATION: 22
263 <223> OTHER INFORMATION: i
265 <220> FEATURE:
W--> 266 <221> NAME/KEY: modified base
267 <222> LOCATION: 28
268 <223> OTHER INFORMATION: i
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Degenerative PCR primer designed based on the seq of
272 conventional
273 7-pass transmembrane receptor proteins which are considered to
274 participate in the proliferation of melanoma
276 <400> SEQUENCE: 6
W--> 277 cccaacgaat tcrtagatsa nnggrttnav rca 33
280 <210> SEQ ID NO: 7
281 <211> LENGTH: 32
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/786,442A

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Input Set : A:\ES.txt

Output Set: N:\CRF3\06222001\I786442A.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:224 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:229 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:234 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:256 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:261 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6